

REMARKS

Claims 33-37, 39, 40 and 52-55 were pending prior to entering the amendments.

The Amendment

SEQ ID NOs: 1-14 are inserted at the end of the specification. These sequences are identical to those sequences submitted in the paper copy and computer-readable format of the sequence listing on July 18, 2007. Applicants submit that the material being inserted is the material previously incorporated by reference and that the amendment contains no new matter (37CFR 1.57(f)).

Claim 33 is amended to recite high grade cervical intraepithelial neoplasia; support for the amendment can be found, for example, page 40, line 5. Claim 33 is also amended to recite that threshold levels of the normalization markers is determined from an adequate and predefined amount of ectocervical cells or endocervical cells; support for the amendment can be found, for example, at page 47, lines 6-19. Claim 33 is further amended to clarify the meaning of the claim. Support for the amendment can be found, for example, at page 47, lines 1-26.

Claim 40 is amended to correct the typographic error of endocervical to ectocervical. Support for the amendment can be found at page 30, lines 5-8 and Table 1.

New Claim 56 is similar to Claim 33 except that it recites determining the presence or absence of a detectable level of at least one normalization marker. Support for the amendment can be found at page 20, lines 24-27.

New Claims 57-62 are similar to Claims 36, 37, 39, 40, 54, and 55.

No new matter is added in any of the amendments. The Examiner is requested to enter the amendment and reconsider the application.

The Response

Objection to Amendment

4. Applicants have amended the specification to insert SEQ ID NOs: 1-14. Applicants submit that the material being inserted is the material previously incorporated by reference and that the amendment contains no new matter (37CFR 1.57(f)).

Objection to the Specification

5. Applicant have properly identified the trademark of HYBOND®.

35 USC §112 Second Paragraph Rejection

7. Claims 33-37, 39, 40 and 52-55 are rejected under 35 U.S.C. §112, second paragraph, as allegedly being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

The Examiner states that it cannot be ascertained how the determination that the sample is adequate, or not, is made by the comparison step; and furthermore, it cannot be ascertained how cervical dysplasia, cervical cancer or cervical intraepithelial neoplasia is detected upon the "basis" of the level of and the adequacy of the sample.

Applicants have amended Claim 33 to recite that threshold levels of the normalization markers is determined from an adequate and predefined amount of ectocervical cells or endocervical cells. At page 47 at lines 9-17, the application describes how to determine a threshold value by measuring the OD value of an adequate and predefined amount of endocervical cells or ectocervical cells. Although the application exemplifies 200,000 squamous ectocervical cells, 2000 columnar endocervical cells and the OD values, it must be understood that the value for the cells as well for OD may vary depending to the reaction conditions. Those of skill in the art know how an appropriate threshold value for a particular test format may be established.

Therefore, the §112 second paragraph rejection should be withdrawn in view of the claim amendment.

35 USC §112 First Paragraph Rejection

9. Claims 33-37, 39, 40 and 52-55 are rejected under 35 U.S.C. §112, first paragraph, as allegedly failing to comply with the written description requirement.

The Examiner states that none of the claims are directed to both a particularly identified "relevant marker" and a particularly identified "normalization marker".

Applicants have amended Claim 33 to identify the relevant marker as p16^{INK4a} and the normalization markers as proteins having SEQ ID NOs:1-12.

10. Claims 33-37, 39, 40 and 52-55 are rejected under 35 U.S.C. §112, first paragraph, because the specification, while being enabling for using a process for diagnosing cervical dysplasia or cervical cancer, said process comprising detecting the level of expression p16^{INK4a}, does not allegedly provide enablement for using a process for diagnosing any type of cervical intraepithelial neoplasia.

Applicants have amended Claim 33 to recite detecting high grade cervical intraepithelial neoplasia.

The Examiner states that a marker that does not distinguish cervical dysplasia, cervical cancer, and cervical intraepithelial neoplasia cannot be expected to be useful in the differential diagnosis of such conditions or diseases.

Applicants respectfully submit that the claims are directed to a method for detecting cervical dysplasia, cervical cancer, or high grade cervical intraepithelial neoplasia, which is a screening method, and is not a method for differential diagnosis.

The Examiner states that the values of the "threshold levels" of the normalization markers to which the claims refer are not known or disclosed.

Applicants have amended the claim to recite how to determine the threshold levels.

35 USC §112 Second Paragraph Rejection

11. Claims 33-37, 39, 40 and 52-55 are rejected under 35 U.S.C. §112, second paragraph, as allegedly being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Applicants have amended the claims to address the issues.

35 USC §112 First Paragraph Rejection

Claims 33-37, 39, 40 and 52-55 are rejected under 35 U.S.C. §112, first paragraph, as allegedly failing to comply with the written description requirement.

Gamma-Catenin, Ep-Cam, E-Cadherin, alpha-1 Catenin, alpha-2 Catenin, beta-Catenin, Involucrin, and p120 are identified in Table 1 by accession numbers. Cytokeratin 8, 18, 10, and 13, p16^{INK4a} and p14ARF are known proteins with well-established sequences. Those skilled in the art would know the exact sequence cytokeratin 8, 18, 10, and 13, p16^{INK4a} and p14ARF. In the Response submitted on July 18, 2007, Applicants have already provided NCBI sequences of the above proteins; each sequence is identified by its name and accession number.

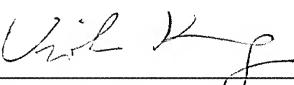
Applicants have amended the specification to insert SEQ ID NOs: 1-14. Applicants submit that the material being inserted is the material previously incorporated by reference and that the amendment contains no new matter (37CFR 1.57(f)).

Conclusion

For all the foregoing reasons, reconsideration of and withdrawal of all outstanding rejections is respectfully requested. The Examiner is earnestly solicited to allow all claims, and pass this application to issuance.

Respectfully submitted,

Date: October 30, 2007



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Enclose: Paper copy of Sequence Listing

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SEQUENCE LISTING

<110> Rudiger Ridder, et.al.

<120> Method for solution based diagnosis

<130> 05033.0003.00US00

<140> 10/633,484

<141> 2003-07-31

<150> EP 02017313.4

<151> 2002-08-01

<160> 14

<170> PatentIn version 3.3

<210> 1

<211> 745

<212> PRT

<213> Homo sapiens

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<223> gamma-Catenin, Swissprot Accession Q86W21

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Cys Gly Arg Gln Tyr Thr Leu Lys Lys Thr Thr Thr Tyr Thr Gln Gly
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Val Pro Pro Ser Gln Gly Asp Leu Glu Tyr Gln Met Ser Thr Thr Ala
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Gln Glu Gly Ala Lys Met Ala Val Arg Leu Ala Asp Gly Leu Gln Lys
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Gly Met Gln Ala Leu Gly Lys His Leu Thr Ser Asn Ser Pro Arg Leu
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Val Gln Asn Cys Leu Trp Thr Leu Arg Asn Leu Ser Asp Val Ala Thr
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Arg His Pro Glu Ala Glu Met Ala	Gln Asn Ser Val Arg Leu Asn Tyr		
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Gly Ile Pro Ala Ile Val Lys Leu	Leu Asn Gln Pro Asn Gln Trp Pro		
485	490	495	
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Cys Glu Leu Ala Gln Asp Lys Glu	Ala Ala Asp Ala Ile Asp Ala Glu		
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Phe Lys His Asp Pro Ala Ala Trp Glu Ala Ala Gln Ser Met Ile Pro
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Ile Asn Glu Pro Tyr Gly Asp Asp Leu Asp Ala Thr Tyr Arg Pro Met
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Tyr Ser Ser Asp Val Pro Leu Asp Pro Leu Glu Met His Met Asp Met
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<213> Homo sapiens

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Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
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Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
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Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
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Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
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Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
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Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
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Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
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Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
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Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
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Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
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Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
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Pro Glu Phe Ser Met Gln Gly Leu Lys Ala Gly Val Ile Ala Val Ile
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Val Val Val Val Met Ala Val Val Ala Gly Ile Val Val Leu Val Ile
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Gly Arg Val Leu Gly Arg Val Asn Phe Glu Asp Cys Thr Gly Arg Gln
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Gly Val Ile Thr Val Lys Arg Pro Leu Arg Phe His Asn Pro Gln Ile
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His Phe Leu Val Tyr Ala Trp Asp Ser Thr Tyr Arg Lys Phe Ser Thr
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Lys Val Thr Leu Asn Thr Val Gly His His His Arg Pro Pro Pro His
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Gln Ala Ser Val Ser Gly Ile Gln Ala Glu Leu Leu Thr Phe Pro Asn
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Asp Gly Ile Leu Lys Thr Ala Lys Gly Leu Asp Phe Glu Ala Lys Gln
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Gln Tyr Ile Leu His Val Ala Val Thr Asn Val Val Pro Phe Glu Val
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Phe Asp Tyr Glu Gly Ser Gly Ser Glu Ala Ala Ser Leu Ser Ser Leu
835 840 845

Asn Ser Ser Glu Ser Asp Lys Asp Gln Asp Tyr Asp Tyr Leu Asn Glu
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Asn Lys Lys Arg Gly Arg Ser Lys Lys Ala His Val Leu Ala Ala Ser
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Val Arg Lys Gln Gly Asp Leu Met Lys Ala Ala Ala Gly Glu Phe Ala
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740 745 750

Gly Ser Arg Met Asp Lys Leu Gly Arg Thr Ile Ala Asp His Cys Pro
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Asp Ser Ala Cys Lys Gln Asp Leu Leu Ala Tyr Leu Gln Arg Ile Ala
770 775 780

Leu Tyr Cys His Gln Leu Asn Ile Cys Ser Lys Val Lys Ala Glu Val
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Gln Asn Leu Gly Gly Glu Leu Val Val Ser Gly Val Asp Ser Ala Met
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Ser Leu Ile Gln Ala Ala Lys Asn Leu Met Asn Ala Val Val Gln Thr
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Val Lys Ala Ser Tyr Val Ala Ser Thr Lys Tyr Gln Lys Ser Gln Gly
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Met Ala Ser Leu Asn Leu Pro Ala Val Ser Trp Lys Met Lys Ala Pro
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Glu Lys Lys Pro Leu Val Lys Arg Glu Lys Gln Asp Glu Thr Gln Thr
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Lys Lys Lys Gly Arg Ser Lys Lys Ala His Val Leu Ala Ala Ser Val
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Glu Gln Ala Thr Gln Asn Phe Leu Glu Lys Gly Glu Gln Ile Ala Lys
65 70 75 80

Glu Ser Gln Asp Leu Lys Glu Glu Leu Val Ala Ala Val Glu Asp Val
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Arg Lys Gln Gly Glu Thr Met Arg Ile Ala Ser Ser Glu Phe Ala Asp
100 105 110

Asp Pro Cys Ser Ser Val Lys Arg Gly Thr Met Val Arg Ala Ala Arg
Page 13

115	120	125
Ala Leu Leu Ser Ala Val Thr Arg Leu Leu Ile Leu Ala Asp Met Ala		
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Lys Glu Phe Gly Lys Glu Met Val Lys Leu Asn Tyr Val Ala Ala Arg		
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370

375

380

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Arg Met Ala Ala Thr Gln Ile Asp Ser Leu Cys Pro Gln Val Ile Asn
450 455 460

Ala Ala Leu Thr Leu Ala Ala Arg Pro Gln Ser Lys Val Ala Gln Asp
465 470 475 480

Asn Met Asp Val Phe Lys Asp Gln Trp Glu Lys Gln Val Arg Val Leu
485 490 495

Thr Glu Ala Val Asp Asp Ile Thr Ser Val Asp Asp Phe Leu Ser Val
500 505 510

Ser Glu Asn His Ile Leu Glu Asp Val Asn Lys Cys Val Ile Ala Leu
515 520 525

Gln Glu Gly Asp Val Asp Thr Leu Asp Arg Thr Ala Gly Ala Ile Arg
530 535 540

Gly Arg Ala Ala Arg Val Ile His Ile Ile Asn Ala Glu Met Glu Asn
545 550 555 560

Tyr Glu Ala Gly Val Tyr Thr Glu Lys Val Leu Glu Ala Thr Lys Leu
565 570 575

Leu Ser Glu Thr Val Met Pro Arg Phe Ala Glu Gln Val Glu Val Ala
580 585 590

Ile Glu Ala Leu Ser Ala Asn Val Pro Gln Pro Phe Glu Glu Asn Glu
595 600 605

Phe Ile Asp Ala Ser Arg Leu Val Tyr Asp Gly Val Arg Asp Ile Arg
610 615 620

Lys Ala Val Leu Met Ile Arg Thr Pro Glu Glu Leu Glu Asp Asp Ser
Page 15

625 630 635 640

Asp Phe Glu Gln Glu Asp Tyr Asp Val Arg Ser Arg Thr Ser Val Gln
645 650 655

Thr Glu Asp Asp Gln Leu Ile Ala Gly Gln Ser Ala Arg Ala Ile Met
660 665 670

Ala Gln Leu Pro Gln Glu Glu Lys Ala Lys Ile Ala Glu Gln Val Glu
675 680 685

Ile Phe His Gln Glu Lys Ser Lys Leu Asp Ala Glu Val Ala Lys Trp
690 695 700

Asp Asp Ser Gly Asn Asp Ile Ile Val Leu Ala Lys Gln Met Cys Met
705 710 715 720

Ile Met Met Glu Met Thr Asp Phe Thr Arg Gly Lys Gly Pro Leu Lys
725 730 735

Asn Thr Ser Asp Val Ile Asn Ala Ala Lys Lys Ile Ala Glu Ala Gly
740 745 750

Ser Arg Met Asp Lys Leu Ala Arg Ala Val Ala Asp Gln Cys Pro Asp
755 760 765

Ser Ala Cys Lys Gln Asp Leu Leu Ala Tyr Leu Gln Arg Ile Ala Leu
770 775 780

Tyr Cys His Gln Leu Asn Ile Cys Ser Lys Val Lys Ala Glu Val Gln
785 790 795 800

Asn Leu Gly Gly Glu Leu Ile Val Ser Gly Thr Gly Val Gln Ser Thr
805 810 815

Phe Thr Thr Phe Tyr Glu Val Asp Cys Asp Val Ile Asp Gly Gly Arg
820 825 830

Ala Ser Gln Leu Ser Thr His Leu Pro Thr Cys Ala Glu Gly Ala Pro
835 840 845

Ile Gly Ser Gly Ser Ser Asp Ser Ser Met Leu Asp Ser Ala Thr Ser
850 855 860

Leu Ile Gln Ala Ala Lys Asn Leu Met Asn Ala Val Val Leu Thr Val
865 870 875 880

Lys Ala Ser Tyr Val Ala Ser Thr Lys Tyr Gln Lys Val Tyr Gly Thr

885

890

895

Ala Ala Val Asn Ser Pro Val Val Ser Trp Lys Met Lys Ala Pro Glu
900 905 910

Lys Lys Pro Leu Val Lys Arg Glu Lys Pro Glu Glu Phe Gln Thr Arg
915 920 925

Val Arg Arg Gly Ser Gln Lys Lys His Ile Ser Pro Val Gln Ala Leu
930 935 940

Ser Glu Phe Lys Ala Met Asp Ser Phe
945 950

<210> 6
<211> 781
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(781)
<223> beta-Catenin, Swissprot Accession P35222

<400> 6

Met Ala Thr Gln Ala Asp Leu Met Glu Leu Asp Met Ala Met Glu Pro
1 5 10 15

Asp Arg Lys Ala Ala Val Ser His Trp Gln Gln Gln Ser Tyr Leu Asp
20 25 30

Ser Gly Ile His Ser Gly Ala Thr Thr Thr Ala Pro Ser Leu Ser Gly
35 40 45

Lys Gly Asn Pro Glu Glu Glu Asp Val Asp Thr Ser Gln Val Leu Tyr
50 55 60

Glu Trp Glu Gln Gly Phe Ser Gln Ser Phe Thr Gln Glu Gln Val Ala
65 70 75 80

Asp Ile Asp Gly Gln Tyr Ala Met Thr Arg Ala Gln Arg Val Arg Ala
85 90 95

Ala Met Phe Pro Glu Thr Leu Asp Glu Gly Met Gln Ile Pro Ser Thr
100 105 110

Gln Phe Asp Ala Ala His Pro Thr Asn Val Gln Arg Leu Ala Glu Pro
115 120 125

Ser Gln Met Leu Lys His Ala Val Val Asn Leu Ile Asn Tyr Gln Asp
130 135 140

Asp Ala Glu Leu Ala Thr Arg Ala Ile Pro Glu Leu Thr Lys Leu Leu
145 150 155 160

Asn Asp Glu Asp Gln Val Val Asn Lys Ala Ala Val Met Val His
165 170 175

Gln Leu Ser Lys Lys Glu Ala Ser Arg His Ala Ile Met Arg Ser Pro
180 185 190

Gln Met Val Ser Ala Ile Val Arg Thr Met Gln Asn Thr Asn Asp Val
195 200 205

Glu Thr Ala Arg Cys Thr Ala Gly Thr Leu His Asn Leu Ser His His
210 215 220

Arg Glu Gly Leu Leu Ala Ile Phe Lys Ser Gly Gly Ile Pro Ala Leu
225 230 235 240

Val Lys Met Leu Gly Ser Pro Val Asp Ser Val Leu Phe Tyr Ala Ile
245 250 255

Thr Thr Leu His Asn Leu Leu His Gln Glu Gly Ala Lys Met Ala
260 265 270

Val Arg Leu Ala Gly Gly Leu Gln Lys Met Val Ala Leu Leu Asn Lys
275 280 285

Thr Asn Val Lys Phe Leu Ala Ile Thr Thr Asp Cys Leu Gln Ile Leu
290 295 300

Ala Tyr Gly Asn Gln Glu Ser Lys Leu Ile Ile Leu Ala Ser Gly Gly
305 310 315 320

Pro Gln Ala Leu Val Asn Ile Met Arg Thr Tyr Thr Tyr Glu Lys Leu
325 330 335

Leu Trp Thr Thr Ser Arg Val Leu Lys Val Leu Ser Val Cys Ser Ser
340 345 350

Asn Lys Pro Ala Ile Val Glu Ala Gly Gly Met Gln Ala Leu Gly Leu
355 360 365

His Leu Thr Asp Pro Ser Gln Arg Leu Val Gln Asn Cys Leu Trp Thr
370 375 380

Leu Arg Asn Leu Ser Asp Ala Ala Thr Lys Gln Glu Gly Met Glu Gly
385 390 395 400

Leu Leu Gly Thr Leu Val Gln Leu Leu Gly Ser Asp Asp Ile Asn Val
405 410 415

Val Thr Cys Ala Ala Gly Ile Leu Ser Asn Leu Thr Cys Asn Asn Tyr
420 425 430

Lys Asn Lys Met Met Val Cys Gln Val Gly Gly Ile Glu Ala Leu Val
435 440 445

Arg Thr Val Leu Arg Ala Gly Asp Arg Glu Asp Ile Thr Glu Pro Ala
450 455 460

Ile Cys Ala Leu Arg His Leu Thr Ser Arg His Gln Glu Ala Glu Met
465 470 475 480

Ala Gln Asn Ala Val Arg Leu His Tyr Gly Leu Pro Val Val Lys
485 490 495

Leu Leu His Pro Pro Ser His Trp Pro Leu Ile Lys Ala Thr Val Gly
500 505 510

Leu Ile Arg Asn Leu Ala Leu Cys Pro Ala Asn His Ala Pro Leu Arg
515 520 525

Glu Gln Gly Ala Ile Pro Arg Leu Val Gln Leu Leu Val Arg Ala His
530 535 540

Gln Asp Thr Gln Arg Arg Thr Ser Met Gly Gly Thr Gln Gln Gln Phe
545 550 555 560

Val Glu Gly Val Arg Met Glu Glu Ile Val Glu Gly Cys Thr Gly Ala
565 570 575

Leu His Ile Leu Ala Arg Asp Val His Asn Arg Ile Val Ile Arg Gly
580 585 590

Leu Asn Thr Ile Pro Leu Phe Val Gln Leu Leu Tyr Ser Pro Ile Glu
595 600 605

Asn Ile Gln Arg Val Ala Ala Gly Val Leu Cys Glu Leu Ala Gln Asp
610 615 620

Lys Glu Ala Ala Glu Ala Ile Glu Ala Glu Gly Ala Thr Ala Pro Leu
625 630 635 640

Thr Glu Leu Leu His Ser Arg Asn Glu Gly Val Ala Thr Tyr Ala Ala
645 650 655

Ala Val Leu Phe Arg Met Ser Glu Asp Lys Pro Gln Asp Tyr Lys Lys
660 665 670

Arg Leu Ser Val Glu Leu Thr Ser Ser Leu Phe Arg Thr Glu Pro Met
675 680 685

Ala Trp Asn Glu Thr Ala Asp Leu Gly Leu Asp Ile Gly Ala Gln Gly
690 695 700

Glu Pro Leu Gly Tyr Arg Gln Asp Asp Pro Ser Tyr Arg Ser Phe His
705 710 715 720

Ser Gly Gly Tyr Gly Gln Asp Ala Leu Gly Met Asp Pro Met Met Glu
725 730 735

His Glu Met Gly Gly His His Pro Gly Ala Asp Tyr Pro Val Asp Gly
740 745 750

Leu Pro Asp Leu Gly His Ala Gln Asp Leu Met Asp Gly Leu Pro Pro
755 760 765

Gly Asp Ser Asn Gln Leu Ala Trp Phe Asp Thr Asp Leu
770 775 780

<210> 7
<211> 585
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(585)
<223> Involucrin, Swissprot Accession P07476

<400> 7

Met Ser Gln Gln His Thr Leu Pro Val Thr Leu Ser Pro Ala Leu Ser
1 5 10 15

Gln Glu Leu Leu Lys Thr Val Pro Pro Pro Val Asn Thr His Gln Glu
20 25 30

Gln Met Lys Gln Pro Thr Pro Leu Pro Pro Pro Cys Gln Lys Val Pro
35 40 45

Val Glu Leu Pro Val Glu Val Pro Ser Lys Gln Glu Glu Lys His Met
50 55 60

Thr Ala Val Lys Gly Leu Pro Glu Gln Glu Cys Glu Gln Gln Gln Lys
65 70 75 80

Glu Pro Gln Glu Gln Glu Leu Gln Gln His Trp Glu Gln His Glu
85 90 95

Glu Tyr Gln Lys Ala Glu Asn Pro Glu Gln Gln Leu Lys Gln Glu Lys
100 105 110

Thr Gln Arg Asp Gln Gln Leu Asn Lys Gln Leu Glu Glu Glu Lys Lys
115 120 125

Leu Leu Asp Gln Gln Leu Asp Gln Glu Leu Val Lys Arg Asp Glu Gln
130 135 140

Leu Gly Met Lys Lys Glu Gln Leu Leu Glu Leu Pro Glu Gln Gln Glu
145 150 155 160

Gly His Leu Lys His Leu Glu Gln Gln Glu Gly Gln Leu Lys His Pro
165 170 175

Glu Gln Gln Glu Gly Gln Leu Glu Leu Pro Glu Gln Gln Glu Gly Gln
180 185 190

Leu Glu Leu Pro Glu Gln Gln Glu Gly Gln Leu Glu Leu Pro Glu Gln
195 200 205

Gln Glu Gly Gln Leu Glu Leu Pro Glu Gln Gln Glu Gly Gln Leu Glu
210 215 220

Leu Pro Gln Gln Gln Glu Gly Gln Leu Glu Leu Ser Glu Gln Gln Glu
225 230 235 240

Gly Gln Leu Glu Leu Ser Glu Gln Gln Glu Gly Gln Leu Glu Leu Ser
245 250 255

Glu Gln Gln Glu Gly Gln Leu Lys His Leu Glu His Gln Glu Gly Gln
260 265 270

Leu Glu Val Pro Glu Glu Gln Met Gly Gln Leu Lys Tyr Leu Glu Gln
275 280 285

Gln Glu Gly Gln Leu Lys His Leu Asp Gln Gln Glu Lys Gln Pro Glu
290 295 300

Leu Pro Glu Gln Gln Met Gly Gln Leu Lys His Leu Glu Gln Gln Glu
305 310 315 320

Gly Gln Pro Lys His Leu Glu Gln Gln Glu Gly Gln Leu Glu Gln Leu
325 330 335

Glu Glu Gln Glu Gly Gln Leu Lys His Leu Glu Gln Gln Glu Gly Gln
340 345 350

Leu Glu His Leu Glu His Gln Glu Gly Gln Leu Gly Leu Pro Glu Gln
355 360 365

Gln Val Leu Gln Leu Lys Gln Leu Glu Lys Gln Gln Gly Gln Pro Lys
370 375 380

His Leu Glu Glu Glu Gly Gln Leu Lys His Leu Val Gln Gln Glu
385 390 395 400

Gly Gln Leu Lys His Leu Val Gln Glu Gly Gln Leu Glu Gln Gln
405 410 415

Glu Arg Gln Val Glu His Leu Glu Gln Gln Val Gly Gln Leu Lys His
420 425 430

Leu Glu Glu Gln Glu Gly Gln Leu Lys His Leu Glu Gln Gln Gln Gly
435 440 445

Gln Leu Glu Val Pro Glu Gln Gln Val Gly Gln Pro Lys Asn Leu Glu
450 455 460

Gln Glu Glu Lys Gln Leu Glu Leu Pro Glu Gln Gln Glu Gly Gln Val
465 470 475 480

Lys His Leu Glu Lys Gln Glu Ala Gln Leu Glu Leu Pro Glu Gln Gln
485 490 495

Val Gly Gln Pro Lys His Leu Glu Gln Gln Glu Lys His Leu Glu His
500 505 510

Pro Glu Gln Gln Asp Gly Gln Leu Lys His Leu Glu Gln Gln Glu Gly
515 520 525

Gln Leu Lys Asp Leu Glu Gln Gln Lys Gly Gln Leu Glu Gln Pro Val
530 535 540

Phe Ala Pro Ala Pro Gly Gln Val Gln Asp Ile Gln Pro Ala Leu Pro
545 550 555 560

Thr Lys Gly Glu Val Leu Leu Pro Val Glu His Gln Gln Gln Lys Gln
565 570 575

Glu Val Gln Trp Pro Pro Lys His Lys
580 585

<210> 8
<211> 483
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(483)
<223> CK8, Swissprot Accession NP_002264

<400> 8

Met Ser Ile Arg Val Thr Gln Lys Ser Tyr Lys Val Ser Thr Ser Gly
1 5 10 15

Pro Arg Ala Phe Ser Ser Arg Ser Tyr Thr Ser Gly Pro Gly Ser Arg
20 25 30

Ile Ser Ser Ser Phe Ser Arg Val Gly Ser Ser Asn Phe Arg Gly
35 40 45

Gly Leu Gly Gly Tyr Gly Ala Ser Gly Met Gly Gly Ile Thr
50 55 60

Ala Val Thr Val Asn Gln Ser Leu Leu Ser Pro Leu Val Leu Glu Val
65 70 75 80

Asp Pro Asn Ile Gln Ala Val Arg Thr Gln Glu Lys Glu Gln Ile Lys
85 90 95

Thr Leu Asn Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe Leu
100 105 110

Glu Gln Gln Asn Lys Met Leu Glu Thr Lys Trp Ser Leu Leu Gln Gln
115 120 125

Gln Lys Thr Ala Arg Ser Asn Met Asp Asn Met Phe Glu Ser Tyr Ile
130 135 140

Asn Asn Leu Arg Arg Gln Leu Glu Thr Leu Gly Gln Glu Lys Leu Lys
145 150 155 160

Leu Glu Ala Glu Leu Gly Asn Met Gln Gly Leu Val Glu Asp Phe Lys
165 170 175

Asn Lys Tyr Glu Asp Glu Ile Asn Lys Arg Thr Glu Met Glu Asn Glu
180 185 190

Phe Val Leu Ile Lys Lys Asp Val Asp Glu Ala Tyr Met Asn Lys Val
195 200 205

Glu Leu Glu Ser Arg Leu Glu Gly Leu Thr Asp Glu Ile Asn Phe Leu
210 215 220

Arg Gln Leu Tyr Glu Glu Glu Ile Arg Glu Leu Gln Ser Gln Ile Ser
225 230 235 240

Asp Thr Ser Val Val Leu Ser Met Asp Asn Ser Arg Ser Leu Asp Met
245 250 255

Asp Ser Ile Ile Ala Glu Val Lys Ala Gln Tyr Glu Asp Ile Ala Asn
260 265 270

Arg Ser Arg Ala Glu Ala Glu Ser Met Tyr Gln Ile Lys Tyr Glu Glu
275 280 285

Leu Gln Ser Leu Ala Gly Lys His Gly Asp Asp Leu Arg Arg Thr Lys
290 295 300

Thr Glu Ile Ser Glu Met Asn Arg Asn Ile Ser Arg Leu Gln Ala Glu
305 310 315 320

Ile Glu Gly Leu Lys Gly Gln Arg Ala Ser Leu Glu Ala Ala Ile Ala
325 330 335

Asp Ala Glu Gln Arg Gly Glu Leu Ala Ile Lys Asp Ala Asn Ala Lys
340 345 350

Leu Ser Glu Leu Glu Ala Ala Leu Gln Arg Ala Lys Gln Asp Met Ala
355 360 365

Arg Gln Leu Arg Glu Tyr Gln Glu Leu Met Asn Val Lys Leu Ala Leu
370 375 380

Asp Ile Glu Ile Ala Thr Tyr Arg Lys Leu Leu Glu Gly Glu Ser
385 390 395 400

Arg Leu Glu Ser Gly Met Gln Asn Met Ser Ile His Thr Lys Thr Thr
405 410 415

Ser Gly Tyr Ala Gly Gly Leu Ser Ser Ala Tyr Gly Gly Leu Thr Ser
420 425 430

Pro Gly Leu Ser Tyr Ser Leu Gly Ser Ser Phe Gly Ser Gly Ala Gly
435 440 445

Ser Ser Ser Phe Ser Arg Thr Ser Ser Ser Arg Ala Val Val Val Lys
450 455 460

Lys Ile Glu Thr Arg Asp Gly Lys Leu Val Ser Glu Ser Ser Asp Val
465 470 475 480

Leu Pro Lys

<210> 9
<211> 430
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(423)
<223> CK18, Swissprot Accession NP_954657

<400> 9

Met Ser Phe Thr Thr Arg Ser Thr Phe Ser Thr Asn Tyr Arg Ser Leu
1 5 10 15

Gly Ser Val Gln Ala Pro Ser Tyr Gly Ala Arg Pro Val Ser Ser Ala
20 25 30

Ala Ser Val Tyr Ala Gly Ala Gly Gly Ser Gly Ser Arg Ile Ser Val
35 40 45

Ser Arg Ser Thr Ser Phe Arg Gly Gly Met Gly Ser Gly Gly Leu Ala
50 55 60

Thr Gly Ile Ala Gly Gly Leu Ala Gly Met Gly Gly Ile Gln Asn Glu
65 70 75 80

Lys Glu Thr Met Gln Ser Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp
85 90 95

Arg Val Arg Ser Leu Glu Thr Glu Asn Arg Arg Leu Glu Ser Lys Ile
100 105 110

Arg Glu His Leu Glu Lys Lys Gly Pro Gln Val Arg Asp Trp Ser His
115 120 125

Tyr Phe Lys Ile Ile Glu Asp Leu Arg Ala Gln Ile Phe Ala Asn Thr
130 135 140

Val Asp Asn Ala Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu Ala
Page 25

145 150 155 160
Ala Asp Asp Phe Arg Val Lys Tyr Glu Thr Glu Leu Ala Met Arg Gln
165 170 175
Ser Val Glu Asn Asp Ile His Gly Leu Arg Lys Val Ile Asp Asp Thr
180 185 190
Asn Ile Thr Arg Leu Gln Leu Glu Thr Glu Ile Glu Ala Leu Lys Glu
195 200 205
Glu Leu Leu Phe Met Lys Lys Asn His Glu Glu Glu Val Lys Gly Leu
210 215 220
Gln Ala Gln Ile Ala Ser Ser Gly Leu Thr Val Glu Val Asp Ala Pro
225 230 235 240
Lys Ser Gln Asp Leu Ala Lys Ile Met Ala Asp Ile Arg Ala Gln Tyr
245 250 255
Asp Glu Leu Ala Arg Lys Asn Arg Glu Glu Leu Asp Lys Tyr Trp Ser
260 265 270
Gln Gln Ile Glu Glu Ser Thr Thr Val Val Thr Thr Gln Ser Ala Glu
275 280 285
Val Gly Ala Ala Glu Thr Thr Leu Thr Glu Leu Arg Arg Thr Val Gln
290 295 300
Ser Leu Glu Ile Asp Leu Asp Ser Met Arg Asn Leu Lys Ala Ser Leu
305 310 315 320
Glu Asn Ser Leu Arg Glu Val Glu Ala Arg Tyr Ala Leu Gln Met Glu
325 330 335
Gln Leu Asn Gly Ile Leu Leu His Leu Glu Ser Glu Leu Ala Gln Thr
340 345 350
Arg Ala Glu Gly Gln Arg Gln Ala Gln Glu Tyr Glu Ala Leu Leu Asn
355 360 365
Ile Lys Val Lys Leu Glu Ala Glu Ile Ala Thr Tyr Arg Arg Leu Leu
370 375 380
Glu Asp Gly Glu Asp Phe Asn Leu Gly Asp Ala Leu Asp Ser Ser Asn
385 390 395 400
Ser Met Gln Thr Ile Gln Lys Thr Thr Arg Arg Ile Val Asp Gly

405

410

415

Lys Val Val Ser Glu Thr Asn Asp Thr Lys Val Leu Arg His
420 425 430

<210> 10
<211> 593
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(584)
<223> CK10, Swissprot Accession P13645
<400> 10

Met Ser Val Arg Tyr Ser Ser Ser Lys His Tyr Ser Ser Ser Arg Ser
1 5 10 15

Gly Gly Gly Gly Gly Gly Gly Cys Gly Gly Gly Gly Gly Val Ser
20 25 30

Ser Leu Arg Ile Ser Ser Ser Lys Gly Ser Leu Gly Gly Gly Phe Ser
35 40 45

Ser Gly Gly Phe Ser Gly Gly Ser Phe Ser Arg Gly Ser Ser Gly Gly
50 55 60

Gly Cys Phe Gly Gly Ser Ser Gly Gly Tyr Gly Gly Leu Gly Gly Phe
65 70 75 80

Gly Gly Gly Ser Phe Arg Gly Ser Tyr Gly Ser Ser Ser Phe Gly Gly
85 90 95

Ser Tyr Gly Gly Ser Phe Gly Gly Gly Ser Phe Gly Gly Gly Ser Phe
100 105 110

Gly Gly Gly Ser Phe Gly Gly Gly Phe Gly Gly Gly Gly Phe Gly
115 120 125

Gly Gly Phe Gly Gly Gly Phe Gly Gly Asp Gly Gly Leu Leu Ser Gly
130 135 140

Asn Glu Lys Val Thr Met Gln Asn Leu Asn Asp Arg Leu Ala Ser Tyr
145 150 155 160

Leu Asp Lys Val Arg Ala Leu Glu Glu Ser Asn Tyr Glu Leu Glu Gly
165 170 175

Lys Ile Lys Glu Trp Tyr Glu Lys His Gly Asn Ser His Gln Gly Glu
180 185 190

Pro Arg Asp Tyr Ser Lys Tyr Tyr Lys Thr Ile Asp Asp Leu Lys Asn
195 200 205

Gln Ile Leu Asn Leu Thr Thr Asp Asn Ala Asn Ile Leu Leu Gln Ile
210 215 220

Asp Asn Ala Arg Leu Ala Ala Asp Asp Phe Arg Leu Lys Tyr Glu Asn
225 230 235 240

Glu Val Ala Leu Arg Gln Ser Val Glu Ala Asp Ile Asn Gly Leu Arg
245 250 255

Arg Val Leu Asp Glu Leu Thr Leu Thr Lys Ala Asp Leu Glu Met Gln
260 265 270

Ile Glu Ser Leu Thr Glu Glu Leu Ala Tyr Leu Lys Lys Asn His Glu
275 280 285

Glu Glu Met Lys Asp Leu Arg Asn Val Ser Thr Gly Asp Val Asn Val
290 295 300

Glu Met Asn Ala Ala Pro Gly Val Asp Leu Thr Gln Leu Leu Asn Asn
305 310 315 320

Met Arg Ser Gln Tyr Glu Gln Leu Ala Glu Gln Asn Arg Lys Asp Ala
325 330 335

Glu Ala Trp Phe Asn Glu Lys Ser Lys Glu Leu Thr Thr Glu Ile Asp
340 345 350

Asn Asn Ile Glu Gln Ile Ser Ser Tyr Lys Ser Glu Ile Thr Glu Leu
355 360 365

Arg Arg Asn Val Gln Ala Leu Glu Ile Glu Leu Gln Ser Gln Leu Ala
370 375 380

Leu Lys Gln Ser Leu Glu Ala Ser Leu Ala Glu Thr Glu Gly Arg Tyr
385 390 395 400

Cys Val Gln Leu Ser Gln Ile Gln Ala Gln Ile Ser Ala Leu Glu Glu
405 410 415

Gln Leu Gln Gln Ile Arg Ala Glu Thr Glu Cys Gln Asn Thr Glu Tyr
420 425 430

Gln Gln Leu Leu Asp Ile Lys Ile Arg Leu Glu Asn Glu Ile Gln Thr
435 440 445

Tyr Arg Ser Leu Leu Glu Gly Glu Gly Ser Ser Gly Gly Gly Gly Arg
450 455 460

Gly Gly Gly Ser Phe Gly Gly Tyr Gly Gly Ser Ser Gly Gly
465 470 475 480

Gly Ser Ser Gly Gly Tyr Gly Gly His Gly Gly Ser Ser Gly
485 490 495

Gly Gly Tyr Gly Gly Ser Ser Gly Gly Ser Ser Gly Gly Gly
500 505 510

Tyr Gly Gly Ser Ser Ser Gly Gly His Gly Gly Ser Ser Ser
515 520 525

Gly Gly His Gly Gly Ser Ser Ser Gly Gly Tyr Gly Gly Ser Ser
530 535 540

Gly Gly Gly Gly Gly Gly Tyr Gly Gly Ser Ser Gly Gly Ser
545 550 555 560

Ser Ser Gly Gly Tyr Gly Gly Ser Ser Ser Gly Gly His Lys
565 570 575

Ser Ser Ser Ser Gly Ser Val Gly Glu Ser Ser Ser Lys Gly Pro Arg
580 585 590

Tyr

<210> 11
<211> 458
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(458)
<223> CK13, Isoform a, Swissprot Accession NP_705694

<400> 11

Met Ser Leu Arg Leu Gln Ser Ser Ser Ala Ser Tyr Gly Gly Phe
1 5 10 15

Gly Gly Gly Ser Cys Gln Leu Gly Gly Gly Arg Gly Val Ser Thr Cys
20 25 30

Ser Thr Arg Phe Val Ser Gly Gly Ser Ala Gly Gly Tyr Gly Gly Gly
35 40 45

Val Ser Cys Gly Phe Gly Gly Ala Gly Ser Gly Phe Gly Gly Gly
50 55 60

Tyr Gly Gly Gly Leu Gly Gly Tyr Gly Gly Leu Gly Gly Gly
65 70 75 80

Phe Gly Gly Gly Phe Ala Gly Gly Phe Val Asp Phe Gly Ala Cys Asp
85 90 95

Gly Gly Leu Leu Thr Gly Asn Glu Lys Ile Thr Met Gln Asn Leu Asn
100 105 110

Asp Arg Leu Ala Ser Tyr Leu Glu Lys Val Arg Ala Leu Glu Glu Ala
115 120 125

Asn Ala Asp Leu Glu Val Lys Ile Arg Asp Trp His Leu Lys Gln Ser
130 135 140

Pro Ala Ser Pro Glu Arg Asp Tyr Ser Pro Tyr Tyr Lys Thr Ile Glu
145 150 155 160

Glu Leu Arg Asp Lys Ile Leu Thr Ala Thr Ile Glu Asn Asn Arg Val
165 170 175

Ile Leu Glu Ile Asp Asn Ala Arg Leu Ala Ala Asp Asp Phe Arg Leu
180 185 190

Lys Tyr Glu Asn Glu Leu Ala Leu Arg Gln Ser Val Glu Ala Asp Ile
195 200 205

Asn Gly Leu Arg Arg Val Leu Asp Glu Leu Thr Leu Ser Lys Thr Asp
210 215 220

Leu Glu Met Gln Ile Glu Ser Leu Asn Glu Glu Leu Ala Tyr Met Lys
225 230 235 240

Lys Asn His Glu Glu Glu Met Lys Glu Phe Ser Asn Gln Val Val Gly
245 250 255

Gln Val Asn Val Glu Met Asp Ala Thr Pro Gly Ile Asp Leu Thr Arg
260 265 270

Val Leu Ala Glu Met Arg Glu Gln Tyr Glu Ala Met Ala Glu Arg Asn
275 280 285

Arg Arg Asp Ala Glu Glu Trp Phe His Ala Lys Ser Ala Glu Leu Asn
290 295 300

Lys Glu Val Ser Thr Asn Thr Ala Met Ile Gln Thr Ser Lys Thr Glu
305 310 315 320

Ile Thr Glu Leu Arg Arg Thr Leu Gln Gly Leu Glu Ile Glu Leu Gln
325 330 335

Ser Gln Leu Ser Met Lys Ala Gly Leu Glu Asn Thr Val Ala Glu Thr
340 345 350

Glu Cys Arg Tyr Ala Leu Gln Leu Gln Gln Ile Gln Gly Leu Ile Ser
355 360 365

Ser Ile Glu Ala Gln Leu Ser Glu Leu Arg Ser Glu Met Glu Cys Gln
370 375 380

Asn Gln Glu Tyr Lys Met Leu Leu Asp Ile Lys Thr Arg Leu Glu Gln
385 390 395 400

Glu Ile Ala Thr Tyr Arg Ser Leu Leu Glu Gly Gln Asp Ala Lys Met
405 410 415

Ile Gly Phe Pro Ser Ser Ala Gly Ser Val Ser Pro Arg Ser Thr Ser
420 425 430

Val Thr Thr Ser Ser Ala Ser Val Thr Thr Ser Asn Ala Ser
435 440 445

Gly Arg Arg Thr Ser Asp Val Arg Arg Pro
450 455

<210> 12
<211> 968
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(968)
<223> p120, Swissprot Accession 060716

<400> 12

Met Asp Asp Ser Glu Val Glu Ser Thr Ala Ser Ile Leu Ala Ser Val
1 5 10 15

Lys Glu Gln Glu Ala Gln Phe Glu Lys Leu Thr Arg Ala Leu Glu Glu
20 25 30

Glu Arg Arg His Val Ser Ala Gln Leu Glu Arg Val Arg Val Ser Pro
35 40 45

Gln Asp Ala Asn Pro Leu Met Ala Asn Gly Thr Leu Thr Arg Arg His
50 55 60

Gln Asn Gly Arg Phe Val Gly Asp Ala Asp Leu Glu Arg Gln Lys Phe
65 70 75 80

Ser Asp Leu Lys Leu Asn Gly Pro Gln Asp His Ser His Leu Leu Tyr
85 90 95

Ser Thr Ile Pro Arg Met Gln Glu Pro Gly Gln Ile Val Glu Thr Tyr
100 105 110

Thr Glu Glu Asp Pro Glu Gly Ala Met Ser Val Val Ser Val Glu Thr
115 120 125

Ser Asp Asp Gly Thr Thr Arg Arg Thr Glu Thr Thr Val Lys Lys Val
130 135 140

Val Lys Thr Val Thr Arg Thr Val Gln Pro Val Ala Met Gly Pro
145 150 155 160

Asp Gly Leu Pro Val Asp Ala Ser Ser Val Ser Asn Asn Tyr Ile Gln
165 170 175

Thr Leu Gly Arg Asp Phe Arg Lys Asn Gly Asn Gly Gly Pro Gly Pro
180 185 190

Tyr Val Gly Gln Ala Gly Thr Ala Thr Leu Pro Arg Asn Phe His Tyr
195 200 205

Pro Pro Asp Gly Tyr Ser Arg His Tyr Glu Asp Gly Tyr Pro Gly Gly
210 215 220

Ser Asp Asn Tyr Gly Ser Leu Ser Arg Val Thr Arg Ile Glu Glu Arg
225 230 235 240

Tyr Arg Pro Ser Met Glu Gly Tyr Arg Ala Pro Ser Arg Gln Asp Val
245 250 255

Tyr Gly Pro Gln Pro Gln Val Arg Val Gly Gly Ser Ser Val Asp Leu
260 265 270

His Arg Phe His Pro Glu Pro Tyr Gly Leu Glu Asp Asp Gln Arg Ser
275 280 285

Met Gly Tyr Asp Asp Leu Asp Tyr Gly Met Met Ser Asp Tyr Gly Thr
290 295 300

Ala Arg Arg Thr Gly Thr Pro Ser Asp Pro Arg Arg Arg Leu Arg Ser
305 310 315 320

Tyr Glu Asp Met Ile Gly Glu Glu Val Pro Ser Asp Gln Tyr Tyr Trp
325 330 335

Ala Pro Leu Ala Gln His Glu Arg Gly Ser Leu Ala Ser Leu Asp Ser
340 345 350

Leu Arg Lys Gly Gly Pro Pro Pro Asn Trp Arg Gln Pro Glu Leu
355 360 365

Pro Glu Val Ile Ala Met Leu Gly Phe Arg Leu Asp Ala Val Lys Ser
370 375 380

Asn Ala Ala Ala Tyr Leu Gln His Leu Cys Tyr Arg Asn Asp Lys Val
385 390 395 400

Lys Thr Asp Val Arg Lys Leu Lys Gly Ile Pro Val Leu Val Gly Leu
405 410 415

Leu Asp His Pro Lys Lys Glu Val His Leu Gly Ala Cys Gly Ala Leu
420 425 430

Lys Asn Ile Ser Phe Gly Arg Asp Gln Asp Asn Lys Ile Ala Ile Lys
435 440 445

Asn Cys Asp Gly Val Pro Ala Leu Val Arg Leu Leu Arg Lys Ala Arg
450 455 460

Asp Met Asp Leu Thr Glu Val Ile Thr Gly Thr Leu Trp Asn Leu Ser
465 470 475 480

Ser His Asp Ser Ile Lys Met Glu Ile Val Asp His Ala Leu His Ala
485 490 495

Leu Thr Asp Glu Val Ile Ile Pro His Ser Gly Trp Glu Arg Glu Pro
500 505 510

Asn Glu Asp Cys Lys Pro Arg His Ile Glu Trp Glu Ser Val Leu Thr
515 520 525

Asn Thr Ala Gly Cys Leu Arg Asn Val Ser Ser Glu Arg Ser Glu Ala
530 535 540

Arg Arg Lys Leu Arg Glu Cys Asp Gly Leu Val Asp Ala Leu Ile Phe
545 550 555 560

Ile Val Gln Ala Glu Ile Gly Gln Lys Asp Ser Asp Ser Lys Leu Val
565 570 575

Glu Asn Cys Val Cys Leu Leu Arg Asn Leu Ser Tyr Gln Val His Arg
580 585 590

Glu Ile Pro Gln Ala Glu Arg Tyr Gln Glu Ala Ala Pro Asn Val Ala
595 600 605

Asn Asn Thr Gly Pro His Ala Ala Ser Cys Phe Gly Ala Lys Lys Gly
610 615 620

Lys Asp Glu Trp Phe Ser Arg Gly Lys Lys Pro Ile Glu Asp Pro Ala
625 630 635 640

Asn Asp Thr Val Asp Phe Pro Lys Arg Thr Ser Pro Ala Arg Gly Tyr
645 650 655

Glu Leu Leu Phe Gln Pro Glu Val Val Arg Ile Tyr Ile Ser Leu Leu
660 665 670

Lys Glu Ser Lys Thr Pro Ala Ile Leu Glu Ala Ser Ala Gly Ala Ile
675 680 685

Gln Asn Leu Cys Ala Gly Arg Trp Thr Tyr Gly Arg Tyr Ile Arg Ser
690 695 700

Ala Leu Arg Gln Glu Lys Ala Leu Ser Ala Ile Ala Asp Leu Leu Thr
705 710 715 720

Asn Glu His Glu Arg Val Val Lys Ala Ala Ser Gly Ala Leu Arg Asn
725 730 735

Leu Ala Val Asp Ala Arg Asn Lys Glu Leu Ile Gly Lys His Ala Ile
740 745 750

Pro Asn Leu Val Lys Asn Leu Pro Gly Gly Gln Gln Asn Ser Ser Trp
755 760 765

Asn Phe Ser Glu Asp Thr Val Ile Ser Ile Leu Asn Thr Ile Asn Glu
770 775 780

Val Ile Ala Glu Asn Leu Glu Ala Ala Lys Lys Leu Arg Glu Thr Gln
785 790 795 800

Gly Ile Glu Lys Leu Val Leu Ile Asn Lys Ser Gly Asn Arg Ser Glu
805 810 815

Lys Glu Val Arg Ala Ala Ala Leu Val Leu Gln Thr Ile Trp Gly Tyr
820 825 830

Lys Glu Leu Arg Lys Pro Leu Glu Lys Glu Gly Trp Lys Lys Ser Asp
835 840 845

Phe Gln Val Asn Leu Asn Asn Ala Ser Arg Ser Gln Ser Ser His Ser
850 855 860

Tyr Asp Asp Ser Thr Leu Pro Leu Ile Asp Arg Asn Gln Lys Ser Asp
865 870 875 880

Lys Lys Pro Asp Arg Glu Glu Ile Gln Met Ser Asn Met Gly Ser Asn
885 890 895

Thr Lys Ser Leu Asp Asn Asn Tyr Ser Thr Pro Asn Glu Arg Gly Asp
900 905 910

His Asn Arg Thr Leu Asp Arg Ser Gly Asp Leu Gly Asp Met Glu Pro
915 920 925

Leu Lys Gly Thr Thr Pro Leu Met Gln Asp Glu Gly Gln Glu Ser Leu
930 935 940

Glu Glu Glu Leu Asp Val Leu Val Leu Asp Asp Glu Gly Gly Gln Val
945 950 955 960

Ser Tyr Pro Ser Met Gln Lys Ile
965

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<213> Homo sapiens

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<221> misc_feature
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<223> p16INK4a, Swissprot Accession P42771

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Met Glu Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
1 5 10 15

Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu
Page 35

20

25

30

Glu Ala Gly Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
35 40 45

Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
50 55 60

Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg
65 70 75 80

Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val
85 90 95

Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg
100 105 110

Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg
115 120 125

Tyr Leu Arg Ala Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg
130 135 140

Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
145 150 155

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<223> p14arf, Swissprot Accession Q8N726

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Met Gly Arg Gly Arg Cys Val Gly Pro Ser Leu Gln Leu Arg Gly Gln
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Glu Trp Arg Cys Ser Pro Leu Val Pro Lys Gly Gly Ala Ala Ala Ala
20 25 30

Glu Leu Gly Pro Gly Gly Glu Asn Met Val Arg Arg Phe Leu Val
35 40 45

Thr Leu Arg Ile Arg Arg Ala Cys Gly Pro Pro Arg Val Arg Val Phe
50 55 60

Val Val His Ile Pro Arg Leu Thr Gly Glu Trp Ala Ala Pro Gly Ala
65 70 75 80

Pro Ala Ala Val Ala Leu Val Leu Met Leu Leu Arg Ser Gln Arg Leu
85 90 95

Gly Gln Gln Pro Leu Pro Arg Arg Pro Gly His Asp Asp Gly Gln Arg
100 105 110

Pro Ser Gly Gly Ala Ala Ala Pro Arg Arg Gly Ala Gln Leu Arg
115 120 125

Arg Pro Arg His Ser His Pro Thr Arg Ala Arg Arg Cys Pro Gly Gly
130 135 140

Leu Pro Gly His Ala Gly Gly Ala Ala Pro Gly Arg Gly Ala Ala Gly
145 150 155 160

Arg Ala Arg Cys Leu Gly Pro Ser Ala Arg Gly Pro Gly
165 170